



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 102806

**TO:** Minh-Tam Davis  
**Location:** CM1/8A01&8E12  
**Art Unit:** 1642  
Sept 6, 2003

**Case Serial Number:** 09/700700

**From:** P. Sheppard  
**Location:** CM1-1E03  
**Phone:** (703) 308-4499  
**sheppard@uspto.gov**

### Search Notes

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STIC-Biotech/Ch mLib

102806

From: Chan, Christina  
Sent: Saturday, August 30, 2003 9:39 AM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09/700700

RECEIVED

SEP - 2 2003

Please ~~rush~~: Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Friday, August 29, 2003 10:49 AM  
To : Chan, Christina  
Subject: Rush search request for 09/700700

1) Please search SEQ ID NO:335 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL\_ID=09439313>

is a continuation in part of 09352616 <snquery.pl?APPL\_ID=09352616>

Which is a continuation in part of 09288946 <snquery.pl?APPL\_ID=09288946>

Which is a continuation in part of 09232149 <snquery.pl?APPL\_ID=09232149>

Which is a continuation in part of 09159812 <snquery.pl?APPL\_ID=09159812>

Which is a continuation in part of 09115453 <snquery.pl?APPL\_ID=09115453>

Which is a continuation in part of 09030607 <snquery.pl?APPL\_ID=09030607>

Which is a continuation in part of 09020956 <snquery.pl?APPL\_ID=09020956>

Which is a continuation in part of 08904804 <snquery.pl?APPL\_ID=08904804>

Which is a continuation in part of 08806099 <snquery.pl?APPL\_ID=08806099>

Leave # 335  
→ 07/14/98 full dict  
Same as # 115  
Leave both filing 8/25/98  
part of # 335  
Do not leave any  
part of # 335

1) Please search SEQ ID NO:1 of the instant application against the sequences of 20030022275 (or US 6617129) and 60/051080

11

STN = 09/105, 470

Thank you.

(MINH TAM DAVIS)

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Point of Contact  
P. Sheppard  
telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 9/6/03  
Date Completed: 9/6/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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**SEQ ID NO:** 3394  
**LENGTH:** 2984  
**TYPE:** DNA  
**ORGANISM:** Homo sapien

Initial Score	=	2984	Optimized Score	=	2984	Significance	=	26.07
Residue Identity	=	100%	Matches	=	2984	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			

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 1880 1890 1900 1910 1920 1930 1940  
 TGAGTGAGCTTGCAGGAAAGGCGCTTAAGCCCTCGGGAGGCCAGCTTCACTGAGGG  
 1950 1960 1970 1980 1990 2000 2010  
 ATGCTTGGGAACCTGTGTTATGCTTCACTGAGGCCAGCTTCACTGAGGG  
 2020 2030 2040 2050 2060 2070 2080  
 ATGCTTGGGAACCTGTGTTATGCTTCACTGAGGCCAGCTTCACTGAGGG  
 2090 2100 2110 2120 2130 2140 2150  
 AGCAGAGGAGAACGAGAACTCTGCTTCACTGAGGCCAGCTTCACTGAGGG  
 2160 2170 2180 2190 2200 2210 2220  
 AGACATAGAAAGAAATGAAACACAACTAACTAAGGAGCTGAGGCCAGCTTCACT  
 2230 2240 2250 2260 2270 2280 2290  
 CCACTACTTAATTCGTTAGTGAGAACCTTCATTCTTATTAGAAGGCGCACCTACTG  
 2310 2320 2330 2340 2350 2360 2370  
 GCGAAATGCCCACATAAGTTAATAGAAGGTTGCCAATTTCACCCATTTCTGGTTGGCTCCAT  
 2380 2390 2400 2410 2420 2430 2440  
 TCCAATGTTCACTGCCACCTGCTGAGCACCGCCGGACTAGGCCACAAAGCAGGGTAGCTGA  
 2450 2460 2470 2480 2490 2500 2510  
 ATGCTTCTGCTTAACTTCTTAAATAGCATTTAGCTGCTGCTGCTCCACTAGTACTCTC  
 2520 2530 2540 2550 2560 2570 2580  
 ATGGCTTCTGCTTAACTTCTTAAATAGCATTTAGCTGCTGCTGCTCCACTAGTACTCTC  
 2590 2600 2610 2620 2630 2640 2650  
 TCCCTCTCTGAAATTCTCACTGCAATTGCAAGGATTACATTCACCTGCTGATGTTTG  
 2530 2540 2550 2560 2570 2580 2590  
 TGTGCAAAAAGAGTGCTTGTAAATTACTGCTGCTGCTGCTCCACTGCTGCTTTC  
 2660 2670 2680 2690 2700 2710 2720  
 TTGGAACATGTCATTAACCATCTGAACTGGTAGAAACATCTGANGAGCTAGTCATCAGCATGAC  
 2730 2740 2750 2760 2770 2780 2790  
 AGGTGAATGGGGTTCTGAGGACATTCAACAGACGGTTCATGTTAAAGTCTGTTAATAGTT  
 2800 2810 2820 2830 2840 2850 2860  
 AGGTGAATGGGGTTCTGAGGACATTCAACAGACGGTTCATGTTAAAGTCTGTTAATAGTT  
 2870 2880 2890 2900 2910 2920 2930  
 GGGTCTCTACATGATAACACACCTGCTCCATCTGTCACATTAAGTCTGTTAATAGTT  
 2940 2950 2960 2970 2980 2990 2990  
 TCTTTATAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA  
 2990 3000 3010 3020 3030 3040 3050  
 TCTTTATAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA  
 3060 3070 3080 3090 3100 3110 3120  
 4. US-09-439-313-334 (1-2984)  
 US-09-352-616A-4 Sequence 434, Application US/09352616A  
 Sequence 434, Application US/09352616A  
 Patent No. 6395278  
 GENERAL INFORMATION:  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Harlocker, Susan Louise  
 APPLICANT: Jiang, Yuqui  
 APPLICANT: Xu, Jiachun  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
 FILE REFERENCE: 210121\_47C8  
 CURRENT APPLICATION NUMBER: US/09/352.616A  
 CURRENT FILING DATE: 1999-07-13  
 NUMBER OF SEQ ID NO: 472  
 SOFTWARE: PastSeq for Windows Version 3.0  
 SEQ ID NO 434  
 LENGTH: 484  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 Initial Score = 358 Optimized Score = 483 Significance = 2.77  
 Residue Identity = 99% Matches = 484 Mismatches = 0  
 Gaps = 2 Conservative Substitutions = 0  
 2430 2440 2450 2460 2470 2480 2490  
 CCAGCACAAAGCAGGGTAGCTGATTGCTTCTGCTCTTACATTCTTAAATAGGATTAGTC  
 2500 2510 2520 2530 2540 2550 2560  
 TCACTCCCTACTGAGACTCTCTCTCCCTCTGATTATTCCTGCAATTGCAATTGCAAGGAT  
 2570 2580 2590 2600 2610 2620 2630  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2640 2650 2660 2670 2680 2690 2700  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2710 2720 2730 2740 2750 2760 2770  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2780 2790 2800 2810 2820 2830 2840  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2850 2860 2870 2880 2890 2900 2910  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2920 2930 2940 2950 2960 2970 2980  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 2990 3000 3010 3020 3030 3040 3050  
 TACACATTCTGAGTGTGATATGTTGGAATTCATCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 3060 3070 3080 3090 3100 3110 3120





LENGTH: 366  
TYPE: DNA  
ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.05  
Residue Identity = 99% Matches = 365 Mismatches = 1  
Gaps = 2 Conservative Substitutions = 0

TCTTACATTCTTTAAATAAGCATTTAGTGCAGTCCTACTGAGTACTCTTCTCCCTCTCG  
2470 2480 2490 2500 2510 2520 2530  
TCTTACATTCTTTAAATAAGCATTTAGTGCAGTCCTACTGAGTACTCTTCTCCCTCTCG  
2470 2480 2490 2500 2510 2520 2530  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
30 40 50 60 70 80 90  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
30 40 50 60 70 80 90  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2960 2970 2980 2990 3000 3010 3020  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
2960 2970 2980 2990 3000 3010 3020  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
3090 3100 3110 3120 3130 3140 3150  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
3090 3100 3110 3120 3130 3140 3150  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
3160 3170 3180 3190 3200 3210 3220  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTACATTTCAGTGATGTTATGGTGCAGAAA  
3160 3170 3180 3190 3200 3210 3220  
X 10 20

ACTTTTCTATGTTGACATATGAG

9. US-09-439-313-335 (1-2984)

Sequence 115, Application US/09232149A

PATENT NO. 645611  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Devin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

FILE REFERENCE: 210121\_428C5  
CURRENT APPLICATION NUMBER: US/09/159, 812A

CURRENT FILING DATE: 1998-09-23

NUMBER OF SEQ ID NOS: 306

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 115

LENGTH: 366

TYPE: DNA

ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.06

Residue Identity = 99% Matches = 365 Mismatches = 1

Gaps = 2 Conservative Substitutions = 0

TCTTACATTCTTTAAATAAGCATTTAGTGCAGTCCTACTGAGTACTCTTCTCCCTCTCG  
2470 2480 2490 2500 2510 2520 2530  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
3060 3070 3080 3090 3100 3110 3120  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
3060 3070 3080 3090 3100 3110 3120  
X 10 20

ACTTTTCTATGTTGACATATGAG

10. US-09-439-313-335 (1-2984)

Sequence 115, Application US/09159812A

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Devin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121\_428C5

CURRENT APPLICATION NUMBER: US/09/159, 812A

CURRENT FILING DATE: 1998-09-23

NUMBER OF SEQ ID NOS: 306

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 115

LENGTH: 366

TYPE: DNA

ORGANISM: Homo sapien

Initial Score = 278 Optimized Score = 364 Significance = 2.06

Residue Identity = 99% Matches = 365 Mismatches = 1

Gaps = 2 Conservative Substitutions = 0

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2470 2480 2490 2500 2510 2520 2530  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2470 2480 2490 2500 2510 2520 2530  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2540 2550 2560 2570 2580 2590 2600  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2610 2620 2630 2640 2650 2660 2670  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2680 2690 2700 2710 2720 2730 2740  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2750 2760 2770 2780 2790 2800 2810  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2820 2830 2840 2850 2860 2870 2880  
X 10 20

AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
AATTAACTTCACTGCAATTGCAAGGATTACATTCACGTGATGTTATGGTGCAGAAA  
2890 2900 2910 2920 2930 2940 2950  
X 10 20

ACTTTTCTATGTTGACATATGAG



240      250      260      270      280      290      300  
 TGCTAAACGAAACCTCTGCATCTGTCACTAAAGCTGACTGAGTTAGTCAGCACCCACCAA  
 310      320      330      340      350      360      X  
 ACTTATTTCTATGTTTGCAACATATGAG

13 . US-09-439-313-335 (1-2984)  
 US-09-030-607 Sequence 207, Application US/09030607

Sequence 207, Application US/09030607  
 Patent No. 6262245

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 224  
 CORRESPONDENCE ADDRESS: FO

ADDRESSEE: SEED and BERRY LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: WA  
 ZIP: 98104

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: 10/121,427C3

APPLICATION NUMBER: US/09/030,607  
 FILING DATE: 23-FEB-1998

CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mak, David J.

REGISTRATION NUMBER: 31,392  
 REFERENCE/DOCKET NUMBER: 210121,427C3

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4300  
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 332 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550      1560      1570      1580      1590      X      1600      1610  
 CCCAAGCTTATCTGCTTGACTTTAAAGTTGGGGCAGTTCTGAATTGGCTAAAGACATGCA  
 TGAATGGCTAAAGAC-TGCA  
 X      10      20

1620      1630      1640      1650      1660      1670      1680  
 TTCTAAACTGCACTCTTCTCTTAAATAATCATGCTTAATCCAACTCTTAAAG  
 TTCTTAACTGCACTCTTCTCTTAAATAATCATGCTTAATCCAACTCTTAAAG  
 30      40      50      60      70      80      90

1690      1700      1710      1720      1730      1740      1750  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC

1690      1700      1710      1720      1730      1740      1750  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC

14 . US-09-439-313-335 (1-2984)

US-09-352-616A-2 Sequence 207, Application US/09352616A

Sequence 207, Application US/09352616A  
 Patent No. 6395278

GENERAL INFORMATION:  
 APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang, Yugu

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

FILE REFERENCE: 210121,427C8

CURRENT APPLICATION NUMBER: US/09/352,616A

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 207  
 LENGTH: 332

TYPE: DNA  
 FEATURE:  
 NAME/KEY: misc\_feature  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1..:(332))  
 OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550      1560      1570      1580      1590      X      1600      1610  
 CCCAAGCTTATCTGCTTGACTTTAAAGTTGGGGCAGTTCTGAATTGGCTAAAGACATGCA  
 TGAATGGCTAAAGAC-TGCA  
 X      10      20

1620      1630      1640      1650      1660      1670      1680  
 TTCTAAACTGCACTCTTCTCTTAAATAATCATGCTTAATCCAACTCTTAAAG  
 TTCTTAACTGCACTCTTCTCTTAAATAATCATGCTTAATCCAACTCTTAAAG  
 30      40      50      60      70      80      90

1690      1700      1710      1720      1730      1740      1750  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC

1690      1700      1710      1720      1730      1740      1750  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC  
 ACCTGACAGCTGAGAAGTCTACTACGCTTAAAGCTGCTCTGCTGTTACGTTGAGTC

1760 1770 1780 1790 1800 1810 1820 1830  
 TGACAATCCTTGAGATCTTCATGCAGGGAGGAGGTTACAGAGGAACACAGC  
 ||||| ||||| |||||  
 TGACAATCCTTGAGATCTTCATGCAGGGAGGAGGTTACAGAGGAACACAGC  
 170 180 190 200 210 220 230  
 ||||| |||||  
 1840 1850 1860 1870 1880 1890  
 GCAG-AATGAA-GGGCAGGTACTTGAGC-TGTCCAGTGGGGCTCATGGGGACATGGAGAAGGG  
 ||||| |||||  
 GCAG-AATGAA-GGGCAGGTACTTGAGC-TGTCCAGTGGGGCTCATGGGGACATGGAGAAGGG  
 170 180 190 200 210 220 230  
 ||||| |||||  
 1900 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTGGCCCTGGAGGCCAGTCACCTGAGCAAGCAAGGACTGAGTGAGCCTTTCAGGAAAGGCT  
 ||||| |||||  
 CAGCTTGGCCCTGGAGGCCAGTCACCTGAGCAAGCAAGGACTGAGTGAGCCTTTCAGGAAAGGCT  
 310 320 330 X  
 ||||| |||||

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15. US-09-439-313-335 (1-2984)  
 US-09-232-149A-2 Sequence 207, Application US/09232149A

Sequence 207, Application US/09232149A  
 Patent No. 6455611  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121-427C6

CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 207

LENGTH: 332

TYPE: DNA  
 ORGANISM: Homo sapien

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(332)

OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

X

10 20

1550 1560 1570 1580 1590 X 1600 1610

10 20

1620 1630 1640 1650 1660 1670 1680

10 20

1690 1700 1710 1720 1730 1740 1750

10 20

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19. US-09-439-313-335 (1-2984)  
US-09-352-616A-2 Sequence 295, Application US/09352616A

Sequence 295, Application US/09352616A  
Patent No. 6355278

GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.

APPLICANT: Jiang, Yuqij

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Xu, Jiangchun

APPLICANT: Billon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Jiang, Yuqij

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Jiang, Yuqij

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Jiang, Yuqij

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121-427C6  
CURRENT APPLICATION NUMBER: US/09/232,149A  
CURRENT FILING DATE: 1999-01-15  
NUMBER OF SEQ ID NOS: 338

SEQUENCE: FastSEQ for Windows Version 3.0

SEQ ID NO: 295

LENGTH: 305

TYPE: DNA

ORGANISM: Homo sapien

Initial Score = 215 Optimized Score = 303 Significance = 1.50  
Residue Identity = 98% Matches = 305 Mismatches = 0  
Gaps = 4 Conservative Substitutions = 0

2460 2470 2480 2490 2500 2510 2520 2530  
GCTCTTACATTTCTTTAAAGCATTTAGTGCTCAGTCCTACTGAGTACTCTTCTCCCTCTC  
GTAACCTCTCTCCCTCCCTC

X GTACCTCTCTCCCTCCCTC  
X 10 20

2540 2550 2560 2570 2580 2590 2600  
TGAATTAACTCTTCACTGCAATTGCAAGGATCACATTCACTGAGTATATGTGTGCAA  
TGAATTAACTCTTCACTGCAATTGCAAGGATCACATTCACTGAGTATATGTGTGCAA  
X 30 40 50 60 70 80 90

2610 2620 2630 2640 2650 2660 2670  
AAAAMAAAGGTCTCTGTAAATTACTGTGTTGATCCATTCTGCTTTCCCATGGACTAG  
AAAAMAAAGGTCTCTGTAAATTACTGTGTTGATCCATTCTGCTTTCCCATGGACTAG  
X 100 110 120 130 140 150 160

2680 2690 2700 2710 2720 2730 2740  
TCATTAACCACTCTGAACTGGTAGAACACATCGAGAGCTGATCTACGAGCTGAGGTGAATTG  
TCATTAACCACTCTGAACTGGTAGAACACATCGAGAGCTGATCTACGAGCTGAGGTGAATTG  
X 170 180 190 200 210 220 230

2750 2760 2770 2780 2790 2800 2810  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X 240 250 260 270 280 290 300

2820 2830 2840 2850 2860  
CATGCATAACAAACCTGCTCCAATGTGTCACATAAAAGCTGTGACTT

X

2890 2900 2910 2920 2930 2940 2950  
CATGCATAACAAACCTGCTCCAATGTGTCACATAAAAGCTGTGACTT

X

2960 2970 2980 2990 3000  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3010 3020 3030 3040 3050 3060 3070  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3080 3090 3100 3110 3120 3130 3140  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3150 3160 3170 3180 3190 3200 3210  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3220 3230 3240 3250 3260 3270 3280  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3290 3300 3310 3320 3330 3340 3350  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3360 3370 3380 3390 3400 3410 3420  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3430 3440 3450 3460 3470 3480 3490  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3500 3510 3520 3530 3540 3550 3560  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3570 3580 3590 3600 3610 3620 3630  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3640 3650 3660 3670 3680 3690 3700  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3710 3720 3730 3740 3750 3760 3770  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3780 3790 3800 3810 3820 3830 3840  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3850 3860 3870 3880 3890 3900 3910  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3920 3930 3940 3950 3960 3970 3980  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

3990 4000 4010 4020 4030 4040 4050  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4060 4070 4080 4090 4100 4110 4120  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4130 4140 4150 4160 4170 4180 4190  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4200 4210 4220 4230 4240 4250 4260  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4270 4280 4290 4300 4310 4320 4330  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4340 4350 4360 4370 4380 4390 4400  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4410 4420 4430 4440 4450 4460 4470  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4480 4490 4500 4510 4520 4530 4540  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4550 4560 4570 4580 4590 4600 4610  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4620 4630 4640 4650 4660 4670 4680  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

4690 4700 4710 4720 4730 4740 4750  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
GATGGTTCTGAGAACATTGACCCAGACAGCCTGTTCTACCTGTTAAATTAGTTGGTTCTA  
X

20. US-09-439-113-335 (1-2984)  
US-09-232-149A-2 Sequence 295, Application US/09232149A  
Sequence 295, Application US/09232149A  
Patient No. 6455611  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer Lynn  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

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TTTTTCGG-TTCTCCCAAGCATTATCTGCTTGACTTAAAGTTRGGGCCAGATCTGATGG  
 TAATGCAGCTGCCACGAGCTT-----TCCGAC--TGGAAAGCGGCCAGTCGAC-GCACGCAATT  
 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420  
 540 550 560 570 580 590 600  
 CTAAGA-CATGCAATTAA-AACTAGCAGCTTATTCTTCTT-TAAAATCATAGCATTA  
 GTAAAGTAGCCGAATTGTCACCACAGCGC-CATCGTCCTCCACTCTGCAAGTGGGGCATGAA  
 2430 2440 2450 2460 2470 2480 2490  
 610 620 630 640 650 660 670  
 ATCCC-AAACCTAA-TAAAGACCTGACGCTTGAAGG-TCACTACTGCAATTAGACCCCTCTGT  
 TGCGCGGATACCGCTGCTGGTTCTCTG---GATGCCGACCGATTGACCTCCGCTAGAACCTCG  
 2500 2510 2520 2530 2540 2550 2560  
 680 690 700 710 720 730 740 750 760 770 780 790 800  
 GGTTCGCTGCTGAGCTGAGCTCTA-CIA-TC-CTTGAGAATTGCGATGAGAGGGTAA---  
 CGTCAGCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 2570 2580 2590 2600 2610 2620 2630  
 810 820 830 840 850 860  
 AGTGGGGGCGATGCTGGGACATGAAA---AGAACGGCAGCTAGG---CCCTGGAGGCCAGT---  
 CAGCATGAGATCCCGCTGGAGTCACTCGCAG-CGGCGTCCGAAAGATGATGCCAACCTTT  
 CATAGAAGG-CGGCGTGG---AATCGAACCTCGTGTGATGCGAGGTTGGGCTGCGTGGGGTCAATTG  
 2640 2650 2660 2670 2680 2690 2700  
 870 880 890 900 910 920 930 940 950 960 970 980 990  
 --CCACTGAG-CAAGC-AAG-GGAC---TCACTGGCTTGGGAAAG-GCTAACAAAGGA-AAA  
 AACCCTAGAGTCCGCTGGAGAAGCTGTCAGAAGGGCATGCGATGCGCTGGAGGGCG  
 2710 2720 2730 2740 2750 2760 2770  
 1000 1010 1020 1030 1040 1050 1060  
 CCCCAAC-AATCGTAACC---TAGACTCTGAGAGATGAGCAGAGCAAGGAACTGGTGTGCTT  
 CGATAACGCTAACGAC---GAGGAAGCGCTGCCCCATCGCCCA-GCTCTCA-GCATATACCGGG  
 2850 2860 2870 2880 2890 2900 2910  
 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190  
 CCATTTCATCTGTTGAGCTTCAAGGCTGTA---GGGGGGAGC-ATTAA---AAAAATGAAACA  
 AGCCAAACGCTATGT---CCTGATAGCTCCACACCCACCGGCCACAGCTGAGTAACAGGG  
 2920 2930 2940 2950 2960 2970 2980  
 1260 1270 1280 1290 1300 1310  
 TTGAGCTGAGA-ACC---TTCTT---TTATAGAAGGGCCGCTACTGTTGGTGCCTAA  
 TGGCGC-CTTGAGCCGCTTCATCCGAGTGTGCTGCTGCA---TGGATGTTGCTGTTGGTGC  
 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110  
 3120 3130 3140 3150 3160 3170 3180  
 1320 1330 1340 1350 1360 1370  
 -TTGCAATGTCATGCCACCTGCTGCTGACACCG-A-C-G-GAGTACTAGCCAG-----CACAAA  
 GGAGCAGGGTAGATGACAGGAGATCCGCCCCGCACTTGCCCAAATACAGCCAGTCCTCCCGCTCA  
 3190 3200 3210 3220 3230 3240 3250  
 1380 1390 1400 1410 1420 1430  
 --GGCGGGT--AGC-CTGAAATTGCTCTGCTCTACAT-TCTTTTAATAA-ASCATT---TAGTC  
 GTGACAGCTGAGCAGCTGCGAAAGAACGCCAGATGCCGGCTGCTCGCTCGCTCG  
 3260 3270 3280 3290 3300 3310 3320  
 1440 1450 1460 1470 1480  
 T-CAGCCTACTGAGTACTCTTCTCCCTCTCTGATTTTCATTCCTTC-RACTTCGAAATTGCA-A  
 TGCAGTCATTAGGGCOC-GGACAGGAGGGCTGACAAAGAACCCGGGCCCTGC-GCTGACGCC  
 3340 3350 3360 3370 3380 3390 3400  
 1510 1520 1530 1540 1550 1560  
 GGATTAC---ACATTCA-CTG-TGA-TCTATATGTTGCTGAGNGAAAGAACAGTCTTGTAA  
 GGAAACGGCGCATGAGGAGCCGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
 3410 3420 3430 3440 3450 3460 3470  
 1570 1580 1590 1600 1610 1620 1630  
 ATTACTGG---TTGTG-AATTCATCTGCTTTCCTCCATGGCATAGTACAGTACATACCCATC-TGA  
 GGGCGGAGACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
 3480 3490 3500 3510 3520 3530 3540  
 1640 1650 1660 1670 1680 1690  
 ACTGGTAAAGAAACCTG---AAGA-GCTACTCTACAGCA-TCTGACGGGATTTGATGTTCT  
 TCAGAT-CTTGTATCCCCTGCCCCATCAGTCTTGGGAAAGAACCCATCCAGTTACTTGAGGGTT  
 3550 3560 3570 3580 3590 3600 3610  
 1700 1710 1720 1730 1740 1750  
 CAGAACCTTCA---CCCA---GACA-GCTGTTCTMCCTCTCTTATAAA---TTAGTTGG  
 OCCAACTTACAGAGGGCCCCAGCTGCAATCCGGTCTGCTGCTGCTGCTGCTGCT  
 3620 3630 3640 3650 3660 3670 3680  
 1760 1770 1780 1790  
 GTCCTCTACATG---CATACTACAC-CCTGC-TCCATCTG---TCA---ACATA-  
 OCTATGCCATGTAACCCACTGCAAGCTACTGCTCTCTGCTGCTGCTGCT  
 3690 3700 3710 3720 3730 3740 3750  
 1800 1810 1820 1830 1840 1850  
 -AAAGCTGAGC-TTGAAGTTTACTGAGC---CCCGCCAACCTTATTCTTCTATGTT-----T  
 CCCAGTACTGACTACATCTCCGGGTCAGCACGTTCTCGGAC-TGGCTTCTACGTTCTGCT  
 3760 3770 3780 3790 3800 3810 3820  
 1860 1870 1880 1890 1900 1910 1920  
 TTGCAACATATGAGTGTGAAATAAGTACCCATGCTTATTAAAAA---NAAAAAAAGG-GGCC  
 TTGCGCCCTGCGCCCTGAGTGTGCTGCTGCA-GTGAAGCTAAACTGCCAAATAGTGTGAC  
 3830 3840 3850 3860 3870 3880 3890  
 1930 X  
 --G-GCCGCCGACTAGTGA  
 TTGCGCCCTGCGCCCTGAGTGTGCTGCTGCA-GTGAAGCTAAACTGCCAAATAGTGTGAC  
 3900 3910 X 3920 3930 3940 3950 3960



CTGAATTAACTCTTCAACTTGCAATTGCAA

5. US-09-700-700-1 (1-1936)  
US-09-105-470B-1 Sequence 1, Application US/09105470B

Initial Score = 42 Optimized Score = 308 Significance = 1.22  
Residue Identity = 47% Matches = 415 Mismatches = 268  
Gaps = 186 Conservative Substitutions = 0

560 570 580 590 600 X 610 620  
TAATACTTAGGAACTCTTATTTCTTCTTAAATACTAGCATTAATCCAAATCCTTAAAGAC  
X 10

630 640 650 660 670 680 690  
CTGACAGCTTCTAGAACGGTCACTACTGCAATTATAGGACCTTCTGCTGCTGTCTGCTG  
OCG-cggccggggggg---CGAACGC-GGAGGGGCC---GCG---CGCCGACCCGCTCCAGGCC  
20 30 40 50 60 70

700 710 720 730 740 750 760  
ACA-ATTCCTGAGAATCTTC-CATCGAGAGGTAAGAGGTATGGATTTCACAGAGAGAC-ACA  
TCACGCTCTCTCATCCAGCACATCTGGG-----GAGGGCGAGGGCAGGGCGCACGGCA  
80 90 100 110 120 130 140

770 780 790 800 810 820 830  
GCGCAGAGATGA-AGGCCAGCTTACTGAGCTG-TCCAGTG-GAGGTCAATGGTGGGACATGAAAGA  
QC-CAGA-GACAGCGCA---CCCGAGCGGAGCAGACGAGC-X 190

840 850 860 870 880 890 900  
AGGAGACCTAGGGCTGGGAGCCCA-GTCCA-CYTAGAGCAGCAGGGACTGAGGCTTGTGAGGA  
ACGGAGCC---GCGCGGGGCGAGAACGACAGCTGAGCA---CCGGCC---GGCGGC-240 250

910 920 930 940 950 960 970  
AAGGGCTAGAAAGGAAACCATCTTAAACACACAGAACT---GTCACAAAGGCTTGGGACTGTGTT  
GAGGCCGAGAGCCTGGCA---GAGACGGAGCCAGA---AGGCACTGGGCTTAT-CGTGGA-CTCTG-  
260 270 280 290 300 310

980 990 1000 1010 1020 1030 1040  
TTATTCCTATATGGTCC-CCAAAATGGCTAACACACAGAACT---GAGACGGAGATGAGCAGAAAGGG  
-AAACACT-TAGGCCCTTCCAA---GGCTTCCCACAAACCC-----TAACAG-CGGCGAGAGG  
320 330 340 350 360 370

1050 1060 1070 1080 1090 1100 1110  
AAATCTGGCTCTCTCCATTTCTCATCTGTTACAGGCTGCTGAGAGGAGACATTAGAAAMA  
CTCCCGAGCTG-CCTTC-TCCCA-CA---CTCAGGATGATCGAGT---TGAAGA---GGA---AG  
380 390 400 410 420

1120 1130 1140 1150 1160 1170 1180  
TGAACACACAAACAATTACTATGAGGTAACTGAGGCCCTGGAGGTCTCTGACTCCACTTAATTCG  
TTTCAGC-CATCAGAGTAC-CTGCGCCCTGA-ACGGG---CCCACTGGC-CAGAACCTCA---AG  
430 440 450 460 470 480 490

1190 1200 1210 1220 1230 1240 1250  
CTGAGGAACTTCTTCAATTGAGGCAAGCTACTGTTGGGCTGAGGAAACCTTCAATTCTTATA  
CTCACCGAG-ACC---CAATG-----GAAG-----ATA-----TGGTCAGAGACAGCTA  
490 500 510 520 530

1270 1280 1290 1300 1310 1320 1330  
AAG-TTAACTAGGAAAGTGGCAATTGCACTTCTGAGGTTGGCTCACATGCAAGTCAATG  
590 600 610 620 630 640 650

AAGACTAAGGAAA---CGAGCTCTC-CCTCGGGGCTSGAGACTTG3---AGA-AAGCACTCTCTTG  
540 550 560 570 580 590

CACGTGCTGACACGGGAGGAC-TAGCCAGCACAAAGGCAGGGTAGCC-TG---AATGCTCT  
C---GGC-CCTGAA---GA---GGGGCTCTCTCCGGGC---CTCCCTGCTCGTGTATAAGCTATCC  
600 610 620 630 640 650

1400 1410 1420 1430 1440 1450 X 1460  
GCTCTTACATTCT-TTAATAATAGCATTTAGCTGCTAGCCCTACTGAGTACTCTCTCTCCCT  
TTACFACCCATACCGTACTGCGTGGGAGCTGAGCTGAGCAG---CTTTRGGTAA  
660 670 680 690 700 X

1470 1480 1490 1500  
CTGAATTAACTCTTCAACTTGCAATTGCAA

6. US-09-700-700-1 (1-1936)

US-09-105-470B-2 Sequence 29, Application US/09105470B

Initial Score = 34 Optimized Score = 229 Significance = 0.71  
Residue Identity = 46% Matches = 294 Mismatches = 0.71  
Gaps = 112 Conservative Substitutions = 0

740 750 760 770 780 790 800  
GGTAAGGTATTGGATTTCACAGAGGAACACAGGCAAGATGAGGGCAGGGCTACTGAGGCTC  
X 10

810 820 830 840 850 860 870  
CACTGGGGGCTCAGGGTGGGAGATGAAAAGA---AGGCACTCTAGGCCCTGGGAGGCCAGTCACG  
---TGGAGGCTTATCTGTTGACTGTGTTGACTTAACTTCAAGGCGCTT---TCCAAGGCTTCCCACACCTA  
20 30 40 50 60 70 80

880 890 900 910 920 930 940  
AGCA---AGCA---AGGG---ACTGAGTGGCTT-TGGAGGAAAGGCTGAGAAAGGAAACCTTCTAA  
AGCAGCGCANAGGCCCTCGAG-CTGCTCTCTCCCAACTCTAGGTGATGAGTGGAGGGAGT-TGAG  
90 100 110 120 130 140 150

940 950 960 970 980 990 1000  
ACACACAGAAACTGCAATGTTGGAGACTGTGTTA-TTGCTTATAATGGTCCCCAAATGGT  
CCATCAAGGAGTCTGTC---GGCCCTGGAC-GGCCACCTGGCCAGAA---CCTCA---GCT  
160 170 180 190 200 210

1010 1020 1030 1040 1050 1060 1070  
AACTGAGTTCAGGAGAATGAGGAGAGGAAATCTGGCTCTCCATTCTCATCTGTAA  
CAGGAGAC-CCA---ACTGAL-GATWTGGTCCAGACAG-----CGCTATAAGCTA-AGCGAAACAG-C  
220 230 240 250 260 270

1080 1090 1100 1110 1120 1130 1140  
TCTCAGGTTGAGCTGGTAGAGGGAGACATTAAGGAAATCTGGCTCTCCATTCTCATCTGTAA  
CTCCCTGGGANCT-----GGGGAGCT-TGGA-----GAAGG-ACTCTCTTGTGNCGGCCCTGGA  
280 290 300 310 320 330

1150 1160 1170 1180 1190 1200 1210  
TGAGGCGCTGGGAGTCTGACTTCAACTTAATTCGTTAGTGGAGAACCTTCAATTCTTATA  
GGAGGC---NTCCCGGGCCNN---CTGGTNCCTGTTAAT---AAC---AGCGA---NCCTTNTAA  
340 350 360 370 380

1230 1240 1250 1260 1270 1280 1290  
GAGGGCGAGCTACTGTTGGCTAACATAGTAAAGTGGCTAACATTACCCAT  
CCCATGNTG-TAANGCTGG-GGC---ANNGGAAGCCAGTTINTGCTTAANGGCCAGTCTCA---  
390 400 410 420 430 440

TTCTCTGGTTGGGCTCCAGATGCCATGCTCAATGCCACGTGCTGCTCACACCGACGGAGTACTAG--C  
 |||||  
 -----GG--TGAACAAC-CATT--AAGCTCAA--AANG-GG--CTTNC-CCCAGGGTGTNCATGAA  
 450 460 470 480 490 500  
 1300 1310 1320 1330 1340 1350 1360  
 CAGCACAAAGGCAGGGT-AGCCGTGATTCCTTCCTGCTTTAGTTGATTGTTAAATAAGCATTTAGTC  
 |||||  
 AAGCACAGGGCAGGTCTAGGAGGAAAGN  
 510 520 530 X  
 1370 1380 1390 X 1400 1410 1420 1430  
 TCAGTCCT  
 1440

7r. US-09-700-700-1 (1-1936)  
US-09-105-470B-3 Sequence 30, Application US/09105470B

	X	AAGCTTAA- AACTGCAA-				
1150	1160	1170	1180	1190	1200	1210
AGGTACGC-GAGGCCGTGGAGTCCTGACTCCACTTAATTCGGTTAGTGAGAACCTTCAATTTC						
AATAGCTTCA- CTTGCGAG-CGATAA- CATTAAAGTGTCCAAATTCGAG-CGATAACAA-TTC	30	40	50	60	70	80
1220	1230	1240	1250	1260	1270	1280
TTCATTAGGAGGCCAGCTTACTGTGGTGGCAAAATTGCCAACATAAGTTAATAGAAAGTTGCCAATT						
ACACATTAAAGAGGAATTACATAG	90	100	110	X		
1290						
CACCC						

9 . US-09-700-700-1 (1-1936) Sequence 28, Application US/09105470B  
 US-09-105470B-2 Sequence 28, Application US/09105470B

Initial Score	Optimized score	Significance
= 25	= 219	= 0.13
Residue Identity =	Matches =	Mismatches =
= 45%	= 276	= 221
Gaps	Conservative Substitutions	
= 96	= 0	

410 420 430 440 450 460 470 480  
 CTTAACTATGCCCTGCCTTATTAGCCGAGATCCTGGCTTTTGTGTTTTTTCGGTCCTCCCC  
 CACCCC  
 1290  
 AAGCTTAAA-AACTGCAA-X  
 10

20 30 40 50 60 70 80  
 1150 1160 1170 1180 1190 1200 1210  
 AGGTACCTGAGGGCTGGAGTCTCTTGACGCCACTTAATTGGCTTAGTGAGAACITTCATT  
 AAATGTTCA- -CTTGAG-CGGATAA- -CAATTAGATGCTACCAATTGAG-CGGATACAA-TTT  
 1220 1230 1240 1250 1260 1270 1280  
 TTTTATTAGAGGGCCAGCTTACTGTTGGTGGCAAAATTGCCAACATAAGTTAATAGAAAGTGGCCATT  
 ACACCTTAAAGAGGGAAATTACATAG  
 90 100 110 X

	850	850	850	870		880	890	900	910
CTAGGCCCTGGGGAGGCCAGTC	CACTGAG	--CA	-AGCA	-AGGACT	TGAGT	GACGCC	TTTG	CAGAAAGGCT	
c-	AGAGCC	--	AGAT	TCAAGGAACTGGGT	ATTCGA	TAGAGC	GTGCCAGA	-CAGT	CTGCAG
20	30	40	50	60	70	80	90	100	110
	920								
AGAAAAGG	--	AAACCATCTAAAC	AACAGAACTG	TCCAATG	TGTTTG	GGAACTG	TGTTATT		
	930	940	950	960	970				
CAGCGCCCTGGGTCA	AC	AC	AC	AC	AC				
90	100	110	120	130	140				
	980	990	1000	1010	1020	1030	1040		
GCCTATAATGGGTCCCA	--	AAATGGTAA	CCPAGACTCAG	GAGAATGAGG	AGAGGAGA	ACAAAGGAGA	ATC		
GCC-A	ATTCCTTGCC	GTGAA	TGGGACTCTTACT	CTTACTCC	AGGTTAT	--	TTTGAGATG	GAGATG	
150	160	170	180	190	200				
	1050	1060	1070	1080	1090	1100	1110		
TGGCTTCCTTCAT	--	TTTCA	TCTGTATTC	CAGGAGCTG	TAGAGGG	GACATTGAA	AAATGA		
AAGTC	ACAGTGATG	TATGCTG	GTTGTC	CCC	--	TGCCCTGT	-G	GGGGATG	AC
210	220	230	240	250	260	270		--	AGAGTATG
	1120	1130	1140	1150	1160	1170	1180	1190	
AAACACAAAC	AACTTA	CTAATGAGG	TACGCTGAG	GCTGGAG	TCTTGACT	CCACTRACT	TAATCCGTT		
GACCA	GACCGAGG	CT	CGCTG	-GG	CATCA	TG-GTCT	-TCTTGAG		
280	290	300	310	X					
	1200	1210	1220						
AGTAGGAAACCTTCA	TTCTT	TATTAGA	GG						

US-09-105-470B-2 Sequence 26, Application US/09105470B

Initial Score =	28	Optimized Score =	54	Significance =	0.32		
Residue Identity =	50% Matches		62 Mismatches	=	50		
Gaps	10	Conservative Substitutions		=	0		
1070	1080	1090	1100	1110	1120	1130	1140
.	TCTGTATCTAGGAGCTGGAGACATTAGAAATAATGAAACACACACAACTACTATG						

400 410 420 430 440 450

US-09-105-470B-3 sequence 24: Application US/09105470B

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980 ATGGCTCTATAATG-GGTCTCCAAAATGGCTAACCGACTTCAGAGAATGAGCAGAGAGAA
990 990 1000 1010 1020 1030 1040 X
ATGGCTCTATAATG-GGTCTCCAAAATGGCTAACCGACTTCAGAGAATGAGCAGAGAGAA

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460		470		480		490
TCTTGCTGCTCCATTTCATTCGTTATCTCAGGTGAGCTGG						
050	1050	1070	1080	1090		

10. US-09-700-700-1 (1-1936)  
US-09-105-470B-1 Sequence 16, Application US/09105470B

Initial Score = 12 Residual Identity = 53% Gaps = 0 Optimized Score = 14 Significance = -0.71% Mismatches = 12% Conservative Substitutions = 0

GCGCTTGGGCTGTGCAATTTTATAGGAACTGGAAAGGCCTCTTCACATTTCCTGGGTG  
 GCGACTTTRACCCAAAAGGCG

X 250      260      270      280      290  
GAGCAATTAGAACCTAGAACTTCCGGCTATCATATACGTA

US-09-105-470B-2 Sequence 20, Application US/09105470B

Gaps = 2 Conservative Substitutions = 0

X CACTGCCGAGTCAACTG--TTC  
10  
20

GGGCCTTGTGAGGAAGGCTAGAAAAACCATCTAAACACAA  
 |||||  
 TTAGA

12. US-03-700-700-1 (1-1935)

12. US-09-700-700-1 (1-1936)  
US-09-105-470B-1 Sequence 15, Application US/09105470B

Initial Score =	11	Optimized Score =	13	Sigma
Residue Identity =	48%	Matches =	13	Mism
Gaps =	0	Conservative Substitutions		

TGCTGTTCAGNAAAAGAAAAGTGTCTTGTTAAATTACTTGTTGTGATCCCTCTTCTTCTC  
 GCGGATCATGCTTCAAGGGTC  
 X 10 20

CCCCATGGAACTAGTCATTAACCCATCTCTGAAGCTGGTAGAAAACATCTGANGA  
|  
CGGAG  
X

13. US-09-700-700-1 (1-1936)

17. US-09-700-700-1 (1-1936)

US-09-105-470B-1 Sequence 17, Application US/09105470B

Initial Score = 9 Optimized Score = 13 Significance = -0.90  
 Residue Identity = 46% Matches = 13 Mismatches = 15  
 Gaps = 0 Conservative Substitutions = 0

1530 1540 1550 1560 1570 1580 1590 1600  
 ATTGIGTTGCAGNGAAAGAAAAAGTGTCTTGTAAATTACTGGTTTGANTCATTGCTT  
 GCAGGATCCATGCTCAGGTT

1610 1620 1630 1640 1650  
 CCCCCATTGGAACTAGTCATAACCCATCTCTGAACGGGAGAAAACATCTGAGA  
 CCGGAG  
 X

18. US-09-700-700-1 (1-1936)

US-09-105-470B-2 Sequence 23, Application US/09105470B

Initial Score = 8 Optimized Score = 8 Significance = -0.96  
 Residue Identity = 53% Matches = 8 Mismatches = 7  
 Gaps = 0 Conservative Substitutions = 0

1300 1310 1320 1330 1340 X 1350 1360  
 TTCTCTGTTGGGTTGGGCTCCACATGCAATGTCATGCCACGGCTGCTCACCGACCGAGACTAGCCA

X |||||  
 ACACATACATGGAGC  
 X 10 X

1370 1380 1390 1400  
 GCACAAAGGCGGGTAGCTGCTCTGCTCTTACA

19. US-09-700-700-1 (1-1936)

US-09-105-470B-2 Sequence 21, Application US/09105470B

Initial Score = 8 Optimized Score = 13 Significance = -0.96  
 Residue Identity = 54% Matches = 13 Mismatches = 11  
 Gaps = 0 Conservative Substitutions = 0

820 830 840 850 860 X 870 880  
 ATGGGTTGGACATGGAAAGAACAGGCAAGCTAGGCCCTGGAGGCCACTGAGGAGGACTGA

X |||||  
 CACTGCCACAGTCACGTTCT  
 X 10 20

890 900 910 920 930  
 GTGAGCCTTGTGAGAAAGGCTAAGAAAAGGAAACCATCTAAACAC  
 GA  
 X



	2050	2060	2070	2080	2090	2100	2110
TG-TGCCCTCCCTAATGAT	350	360	370	380	390	400	
TCCTTCCATTTCATTCGTTA	2120	2130	2140	2150	2160	2170	2180
AACACTT-CT--TTCNCGTA-NCT-TGANTCTGTATTCAGGA-NCAGCGGATGGATGGC	410	420	430	440	450	460	
AACTATTTAATGAGGTTAGGCTGAGGCCTGGAGCTCTGACTCCCTACTTAATTCGG-TTTAGCTGAG-	2190	2200	2210	2220	2230	2240	2250
CAGCCCNCGGATGTCANT	470	480	X				
AAACCTTCAATTCTTTATTAGAACGGCCAGCTTACTGTTGGCAAAATTGCCAACATAAGTTAA	2260	2270	2280	2290	2300	2310	2320